

Group A10 Sequences

HPV6	HPV11
HPV13	HPV44
HPV55	PCPV1

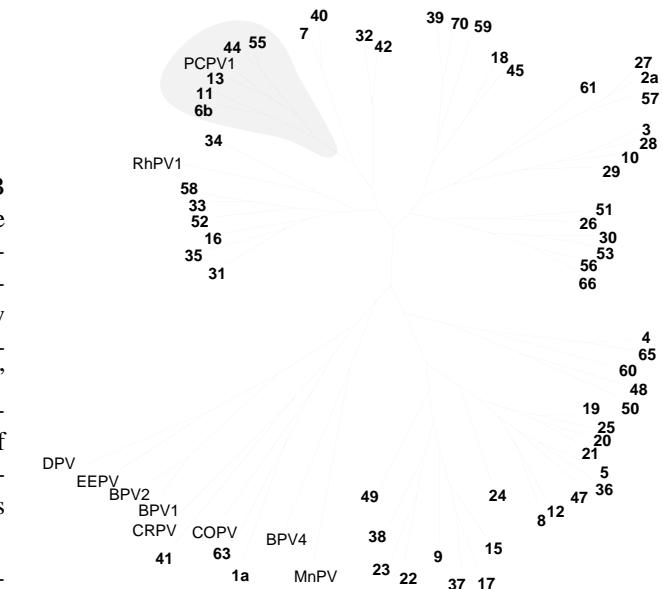
INTRODUCTION

Group A10 includes several of the old group B viruses with the addition of the Pygmy Chimpanzee papillomavirus (PCPV-1). It consists of human papillomavirus types 6, 11, 13, 44, and 55, viruses primarily associated with orogenital lesions with low oncogenic potential, and PCPV-1. Lorinz et al. classified HPV-6, HPV-11 and HPV-44 as “low risk” viruses [1]. DNA from these three viruses and others in the low-risk class was detected in 20.2% of the low-grade cervical lesions, in 4.2% of the high-grade lesions, and in none of the 153 invasive cancers screened [1].

Many researchers view HPV-6 and HPV-11 together as a functional group [1]. These two viruses are primarily responsible for the benign HPV infection of the anogenital tract. Condylomata acuminata have been shown to harbour HPV-6 or HPV-11 DNA in more than 93% of the cases [1]. Conversely, relatively few HPV-6 and HPV-11 positive genital malignancies have been identified despite extensive international screening. In the IBSCC worldwide investigation of over 1000 cervical tumors, a single HPV-6 and a single HPV-11 were identified [2]. Two cases containing HPV-55 were also identified in this study. One type of malignancy, although rare, is strongly correlated with HPV-6 and HPV-11 infection: Buschke-Lowenstein tumors, the highly differentiated squamous cell tumors of the genital region, are associated almost exclusively with HPV-6 and HPV-11 [3,4]. HPV-44 and HPV-55 have been detected in condyloma acuminata of the genital region (vulvar and penile, respectively) [5,6].

The strong association of HPV-6 and HPV-11 with certain types of genital carcinomas (vulvar and vaginal) appears to be inconsistent with their classification as low-risk. Several explanations have been proposed to explain this anomaly. First, Lorincz et al. suggest the limited number of papillomavirus probes available to researchers may have contributed to the false-positive identification of HPV-6 and HPV-11 [1]. Second, researchers have shown a correlation between oncogenic potential and the presence of a duplicate upstream regulatory region in the genome. A species of HPV-11 with this duplication has been shown to transform baby rat kidney cells and such duplications have been found in carcinomas harbouring HPV-11 and HPV-6 DNA [7–10]. However, alterations in the URR should be considered with caution since rearrangements have been observed following amplification of cloned genomes [11]. Recent investigations suggest that rearrangement of the HPV-6b URR occurred during propagation in *E. coli* [12]. Rubben et al. suggest that cellular and environmental factors following infection may induce this duplication event and/or other rearrangements leading to acquired oncogenic properties [10]. Cofactors which may contribute to malignancy include alcohol and tobacco use and sexual intercourse during menstrual periods [13, 14].

In addition to their involvement with anogenital tract lesions, HPV-6, HPV-11 and HPV-13 are strongly associated with ororespiratory tract infection. In one study, 72% of all laryngeal papillomas and 25% of all oral papillomas were positive for HPV-6 and HPV-11 DNA [15]. HPV-6 and HPV-11 have been detected in benign papillomas infecting almost every epithelial lining of the upper digestive and respiratory tracts. These tissues include the larynx, sinonasal area, lung,



tonsil, tongue, and linings of the oral cavity [7, 15–17]. Unexpectedly, a high percentage (60%) of laryngeal carcinomas have been shown to be positive for HPV-11 DNA [18]. HPV-13 was reported by de Villiers to be present in 13% of all oral papillomas [15]. Specifically, HPV-13 has been highly correlated with oral focal epithelial hyperplasia (FEH), a benign lesion situated primarily on the mucosae of the lower lips and cheeks [19]. This disease is frequently found among Indians in Central and South America and in Eskimos in Greenland and Alaska [19]; the prevalence among Caucasians in the same area is much lower [19]. HPV-13 has also been detected in a case of low-grade cervical dysplasia and in Bowenoid papulosis in an HIV-positive male [19].

Several subtypes of HPV-6 have been identified. Subtype 6a has been isolated from tonsillar carcinoma, lung carcinoma and Buschke-Lowenstein tumors [9,16,20]. The complete genomic sequence of HPV-6a has recently been reported (GenBank accession L41216) [21]. As this variant is so similar to the sequence we published last year (HPV-6b) we have chosen not to print it in hard copy form but to make it available on our World Wide Web site (see Part V). HPV-6b, the prototypical HPV-6 subtype, was initially cloned and sequenced from a benign genital wart [22]. It has been subsequently detected in various genital and upper digestive and respiratory tract lesions. The HPV-6c genome was molecularly cloned from both a respiratory-tract papilloma and a condyloma acuminatum of the cervix [23]. This subtype has also been detected in benign laryngeal papillomas and benign nasopapillomas [24]. The HPV-6d genome, cloned from Buschke-Lowenstein tumors, contains a tandem duplication of 459 base pairs in the noncoding region of the genome [16]. HPV-6e was identified in a genital wart and laryngeal papillomas [23–25]. HPV-6f has been cloned from a benign laryngeal papilloma and a non-inverted nasal papilloma [24, 26]. HPV-6vc was cloned from a rapidly growing vulvar verrucous carcinoma [27]. And, finally, a worldwide study of sequence variation in the HPV-6 and HPV-11 URR demonstrating the phylogenetic spectrum of these viruses has been reported [11]; it is perhaps worth noting that the levels of sequence diversity observed in this study are more consistent with considering HPV-6a and HPV-6b to be variants rather than distinct subtypes.

With the release this year of sequences for HPV-44 and HPV-55, complete genomic sequences are now available for all members of Group A10. We consider HPV-11 and HPV-6b to be “close types”—sequences which qualify to be distinct types under the criterion of ten percent dissimilarity at the nucleotide level, but between which most of the changes are “silent”, causing no difference at the amino acid level *Human Papillomaviruses 1994* (Part III). The Pygmy Chimpanzee papillomavirus (PCPV-1), which in last year’s compendium was included in the old group “I,” is close enough to HPV-13 for these to be considered “close types.” A sequence related to PCPV-1 has been identified in a buccal scrape from a chimpanzee (*Pan troglodytes*; like the reference sequence, the variant is more similar to HPV-13 than many HPV types are to each other [28].

What's new?

The complete genomes of HPV-44 and HPV-55 are the only new sequences in Group A10 released during 1995. The sequences of other members of this group were published in *Human Papillomaviruses 1994* pp. I-B-5, I-B-10, and I-B-14.

References

- [1] Lorincz,A.T., Reid,R., Jenson,A.B., Greenberg,M.D., Lancaster,WD, and Kurman,R.J. Human papillomavirus infection of the cervix: relative risk associations of 15 common anogenital types. *Obestet Gynecol* **79**:328–337
- [2] Bosch, F.X., Manos, M.M., Munoz, N., Sherman, M., Jansen, A.M., Peto, J., Schiffman, M.H., Moreno, V., Kurman, R., Shah, K.V., International Biological Study on Cervical Cancer (IBSCC) Study Group. Prevalence of human papillomavirus in cervical cancer: a worldwide perspective. *J Natl Cancer Inst* **87**:796–801 (1995)

- [3] Gissmann,L., deVilliers,E.M., and zur Hausen, H. Analysis of human genital warts (condylomata acuminata) and other genital tumors for human papillomavirus type 6 DNA. *Int J Cancer* **29**:143–6 (1982)
- [4] Lehn, H., Ernst,T.M., and Sauer,G. Transcription of episomal papillomavirus DNA in human condylomata acuminata and Buschke-Lowenstein tumours. *J Gen Virol* **65**:2003–10 (1984)
- [5] Lorincz,A.T., Quinn,A.P., Goldsborough,M.D., Schmidt,B.J., and Temple, G.F. Cloning and partial DNA sequencing of two new human papillomavirus types associated with condylomas and low-grade cervical neoplasia. *J Virol* **63**: 2829–34 (1989)
- [6] Favre,M., Kremsdorf,D., Jablonska,S., Obalek,S., Pehau-Arnaudet,G., Croissant, O., and Orth,G. Two new human papillomavirus types (HPV54 and 55) characterized from genital tumours illustrate the plurality of genital HPVs. *Int J Cancer* **45**:40–6 (1990)
- [7] DiLorenzo,T.P., Tamsen,A., Abramson,A.L., and Steinberg,B.M. Human papillomavirus type 6a DNA in the lung carcinoma of a patient with recurrent laryngeal papillomatosis is characterized by a partial duplication. *J Gen Virol* **73**:423–8 (1992)
- [8] Rosen,M. and Auborn,K. Duplication of the upstream regulatory sequences increases the transformation potential of human papillomavirus type 11. *Virology* **185**:484–7 (1991)
- [9] Boshart,M. and zur Hausen,H. Human papillomaviruses in Buschke-Lowenstein tumors: physical state of the DNA and identification of a tandem duplication in the noncoding region of a human papillomavirus 6 subtype. *J Virol* **58**:963–6 (1986)
- [10] Rubben,A., Beaudenon,S., Favre,M., Schmitz,W., Spelten,B., and Grussendorf-Conen,E.I. Rearrangements of the upstream regulatory region of human papillomavirus type 6 can be found in both Buschke-Lowenstein tumours and in condylomata acuminata. *J Gen Virol* **73**:3147–53 (1992)
- [11] Heinzel,P.A., Chan,S.-Y., Ho,L., O'Connor,M., Balaram,P., Campo,M.S., Fuhinaga,K., Kiviat,N., Kuypers,J., Pfister,H., Steinberg,B.M., Tay, S.-K., Villa,L.L., Bernard,H.-U. Variation of human papillomavirus type 6 (HPV-6) and HPV-11 genomes sampled throughout the world. *J Clinical Micro*, In press (1995)
- [12] Kasher,M.S., Roman,A. Alterations in the regulatory region of the human papillomavirus type 6 are generated during propagation in Escherichia coli. *J Virol* **62**:3295–3300 (1989)
- [13] Rohan,T., Mann,V., McLaughlin,J., Harnish,D.G., Yu,H., Smith,D., Davis,R., Shier,R.M., and Rawls,W. PCR-detected genital papillomavirus infection: prevalence and association with risk factors for cervical cancer. *Int J Cancer* **49**:856–60 (1991)
- [14] Woods,K.V., Shillitoe,E.J., Spitz,M.R., Schantz,S.P., and Adler-Storthz, K. Analysis of human papillomavirus DNA in oral squamous cell carcinomas. *J Oral Pathol Med* **22**:101–8 (1993)
- [15] de Villiers,E.M., Weidauer,H., Le,J.Y., Neumann,C., and zur Hausen, H. Papilloma viruses in benign and malignant tumors of the mouth and upper respiratory tract. *Laryngol Rhinol Otol (Stuttg)* **65**:177–9 (1986)
- [16] Kashima,H.K., Kessis,T., Hruban,R.H., Wu,T.C., Zinreich,S.J., and Shah,K.V. Human papillomavirus in sinonasal papillomas and squamous cell carcinoma. *Laryngoscope* **102**:973–6 (1992)
- [17] Naghashfar,Z., Sawada,E., Kutcher,M.J., Swancar,J., Gupta,J., Daniel, R., Kashima,H., Woodruff, J.D., and Shah,K. Identification of genital tract papillomaviruses HPV-6 and HPV-16 in warts of the oral cavity. *J Med Virol* **17**:313–24 (1985)
- [18] Syrjanen,S., Syrjanen,K., Mantyjarvi,R., Collan,Y., and Karja,J. Human papillomavirus DNA in squamous cell carcinomas of the larynx demonstrated by in situ DNA hybridization. *ORL J Otorhinolaryngol Relat Spec* **49**:175–86 (1987)
- [19] Van Ranst,M., Fuse,A., Fiten,P., Beuken,E., Pfister,H., Burk,R.D., and Opdenakker,G. Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: comparison of the genome organizations. *Virology* **190**:587–96 (1992)

- [20] Kahn.T., Turazza,E., Ojeda,R., Bercovich,A., Stremlau,A., Lichter,P., Poustka,A., Grinstein,S., and zur Hausen,H. Integration of human papillomavirus type 6a DNA in a tonsillar carcinoma: chromosomal localization and nucleotide sequence of the genomic target region. *Cancer Res* **54**:1305–12 (1994) [21] Hoffman, K.j., Cook,J.C., Joyce,J.G., Brown,D.R., Schultz,L.D., George,H., Rosolowsky,M., Fife,K.H., Jansen,K.U., Sequence determination of human papillomavirus type 6a and assembly of virus-like particles in *Saccharomyces cerevisiae*. *Virology* **209**:506–518 (1995)
- [22] de Villiers,E.M., Gissmann,L., and zur Hausen,H. Molecular cloning of viral DNA from human genital warts. *J Virol* **40**:932–935 (1981)
- [23] Metcalfe,L., Chen,S.L., and Mounts,P. Structural analysis of human papillomavirus type 6c isolates from condyloma acuminatum and juvenile-onset and adult-onset laryngeal papillomata. *Virus Genes* **3**:11–27 (1989)
- [24] Ward,P. and Mounts,P. Heterogeneity in mRNA of human papillomavirus type-6 subtypes in respiratory tract lesions. *Virology* **168**:1–12 (1989)
- [25] Ishibashi,T., Tsunokawa,Y., Nomura,Y., Miyata,M., Terada,M. Molecular cloning and characterization of a new subtype of human papillomavirus 6 DNA. *Eur Arch Otorhinolaryngol* **248**:205–8 (1991)
- [26] Ogura,H., Kawakami,T., Fujiwara,T., Sakai,A., Saito,R., Watanabe,S., Masuda,Y., and Yabe,Y. Detection of human papillomavirus type 6f genome in nasal papillomatosis. *Acta Otolaryngol (Stockh)* **112**:115–9 (1992)
- [27] Rando,R.F., Sedlacek,T.V., Hunt,J., Jenson,A.B., Kurman,R.J., and Lancaster,W.D. Verrucous carcinoma of the vulva associated with an unusual type 6 human papillomavirus. *Obstet Gynecol* **67**:70S–75S (1986)
- [28] Eriksson,A., and Wheeler,C.M. personal communication (1995)

HPV44

LOCUS HPV44 7833 bp DNA VRL 18-JUL-1995
DEFINITION Human papillomavirus type 44, complete genome.
ACCESSION U31788
KEYWORDS .
SOURCE Human papillomavirus type 44.
REFERENCE 1 (bases 1 to 7833)
AUTHORS Delius,H.
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,
I.N.F. 506, W-6900 Heidelberg, Germany
REFERENCE 2 (bases 1 to 7833)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,
Los Alamos National Laboratory, T-10, Mail Stop K710, Los Alamos,
NM 87501, USA
COMMENT HPV-44 is a mucosatropic HPV which to date has not been detected in
cervical cancer. Prevalence studies indicate that HPV-44 and HPV-43
have been found in 4% of cervical intraepithelial neoplasms, but in
none of the 56 cervical cancers tested (Lorincz et al, J. Virol 63,
2829-2834). During the analysis of approximately 1000 anogenital
tissue samples, two new HPV types, HPV-43 and HPV-44, were
identified. The complete genome of HPV-44 was recovered from a
vulvar condyloma and cloned into bacteriophage lambda. The biopsy
was taken from a woman from the Detroit Michigan area. The DNA
recovered was a single 7.8 kb BamHI fragment. A possible feature of
HPV types associated with malignant lesions is the potential to
produce a different E6 protein by alternative splicing. This
potential has been found in types HPV-16, HPV-18, and HPV-31.
HPV-44 has a potential E6 splice donor at nt 229, but does not
contain a potential splice acceptor. Phylogenetic analysis
indicates that HPV-44 is most closely related to HPV-55, HPV-6,
HPV-11 and HPV-13.
BASE COUNT 2383 a 1545 c 1678 g 2227 t
ORIGIN 105 bp upstream from beginning of E6 cds
1 ttaataataa tctaaccctt acaaaaaaga ggaggaACCG AATTGGTtc caACCGAAAA
E2 binding -> E2 binding ->
61 CGGTTATATA Aaaaccagcc caaaaattaa gcaagcgggg cataATGcaa agtgcaaatg
E6 orf start -> E6 cds ->
signal ->
121 cctccacgtc tgcacaaagt atagaccagt tgtgcaagga gtgcaacatt cctatgcaca
181 atctgcaaat ttatgcgtg ttttcagaa aaacgttaag tactgcagag gtttattcat
241 tcgcatataa acagtttatgtatgttacc gaggaaactt tccatttgca gcctgtgcc
301 ttgtttaga actacaaggt aaggtaatc aatttaggca tttaactac gcgggatatg
361 cagtaacagt ggaagaagaa acaaataagt caattctgga cgtgctgata cgctgctatt
421 tgtgccacaa accattgtgc cacgtggaaa aggtgcgcca catattggac aaggcgcgat
481 tcattAAatt acaagatACC TGGAAGGGTc gctgttcca ttgtggaca tcATGcatgg
E7 orf start -> -> E2 binding E7 cds ->
541 aaactataact acctTAAagg aaattgtttt acagctggaa cctcctgacc ctgtaggcct
<- E6 end
601 acattgcaat gagcaattag acagctcaga agatgagggtg gatgaactag ccacgcaagc
661 cacgcaagac gttacacagc cttacaaat agtaACCACC TGTGGTACAT gTAGtcggaa
E2 binding -> E1 orf start ->
721 ggttcggctg gttgtgcagt gcacaggaac agacatccat cacctacata cgcttctgct
781 ggttcactg gatatattgt gtcctgtgtg tgcccccggaaa accTAACAac gATGgctgac
<- E7 end
E1 cds ->
841 aatacaggta cagagggAAC gggatgctca ggatggtttc tagtagaggc tatagtggag
901 aacacaaccg ggcaacaat atcagaggat gaggatgagg cagtggagga tagtgggttg

961 gatatggtgg actttataga tgacaggcct attacacaca attccatgga agcacaggca
 1021 ttgttaacg agcaggaggc ghatgctcat tatgcggctg tgcaggacct aaaacgaaag
 1081 tatttagtta gtccatatgt tagtccttta agtaatattt agcaggcagt ggagtgtgac
 1141 attagcccac ggctggacgc tataacatta agtagacaac caaaaaaaagt aaagcgacgg
 1201 ctgtttgaca gaccagaatt aacggacagt ghatatggca atactgaagt ggaagctgaa
 1261 acgcaggtag agagaaatgg cgaaccggaa gattgtgggg gaggtggaca aggaagggac
 1321 acagaggggg tggAACAGGT ggaaacggaa gtgcagacac atagcaacac acaacagcac
 1381 accgggacca cgcgggtact agaactattt aatgttAAGA atataagggc tacactgctt
 1441 ggttaagttt aggattgcta tgggttatca tatacagatt taatttagaca attaaaaagt
 1501 gacaagacaa catgtgggaa ctggtaatt gcagcccttgg ggtgcacca tagtgtgtca
 1561 gaggcggttc aaaatttaat acagccagta acaacatata gccacataca atggcttaca
 1621 aatgcattttt gatggctt actggcatta gtaaggttt aggttAAaa aaacagatgt
 1681 acagtggcac gtatgtggc aaccgttta aatatacctg aggacacat gtaattgaa
 1741 cctcctaaaa tacaagcgg tggcagcg ttatattgg ttagaagtgg tatattccat
 1801 gccagtatag taactggaga aacaccggaa tggataacaa ggcaaacat tggtaacat
 1861 gggcttgca gcaaccaatt taaatttagca gacatggttc aatggcata tgataatgac
 1921 ttttgtgagg aaagtgaat tgcatttga tatgcacaaac gtgcagatat agatgccaat
 1981 gccagagcat tcctaaatag taattgtcag gcaaaatatg taaaagactg tgccacaatg
 2041 tgcaggact ataaaactgc agaaatggaa aaaaatgata tggaaacagtg gataaaattt
 2101 aggaggacta aatttgaaga cacaggaaat tggaaaccaa tagtgcattt ttaagacac
 2161 caaaacatag aatttattcc gtttttaact aaattaaaga tggctgtca tggtacacca
 2221 aaaaaaaaaact gtattgcaat agtggggcca ccagacacag gtaaatcggt tttttgtatg
 2281 agtttaatta aattcttagg aggcactgta attagttatg taaactccag cagtactt
 2341 tggctacagc ccttatgca tgcaaaagta gcattattag atgatgtaac ccaatcctgc
 2401 tgggtatata tggatacata tatgagaaac ctattagatg gaaaccctat gaccattgac
 2461 agaaaacaca aatcattagc attaataaaaa tggccgcctt taatagtaac atcaaacata
 2521 gacattacta aagaagagaa atacaatattt ttagttagca gggtaacattt attacattt
 2581 ccaaatccat tcccccttga cagaaatggg aatgcactat atgactgtg tggaaacaaac
 2641 tggaaatgtt tctttgcaag attatcatca agtcTAGata tacaaacatc agaggacgag

E2 orf start ->

2701 gacgATGgag acaatagcca agcatttga tggctgtccag gaacagttgt tagaactgta
 E2 cds ->

2761 TGAaaaaat agtaataaac ttacaaaaca tatacaacat tggaaatgtt tacgatatga
 <- E1 end

2821 atgtgtgttta ctacacaaag ctaagcaat gggcctgaac cacattggaa tgcagggt
 2881 gcagcatttta gcagtgtcac agacaaaggg acaccaggca attgaaatgc aatgacatt
 2941 agaaacatttta ctaaactctg actatggtac ggaaccatgg acattgcaag agacaagtcg
 3001 gggaaatgtgg ttaacaccac ccaaatattt cttttttttt cagggacaaa ctgtggaaagt
 3061 aaaatttgac tgcatttgc acaatgcaat ggatgttgc tggtaaaag tcattttatgt
 3121 atttgacaca gacaaatggg taaaatgtac aggacacata Gactataaag gttgttatta

E4 orf start ->

NH₂ terminus unknown

3181 tgcattttttt gggcataaaaa cctattatac aaatttttggaa aaggaggccg aaaaatatgg
 3241 gaactcttta caatgggagg tatgtattgg cagcagtttccat atatgttctc ctgcatttat
 3301 atcttagtact tgcaggact tatccattgc tggcctgtc tcacactctt cctcctccac
 3361 caccaccacc cttgcacagg cctcatccac actgcccatt ggcaccggc aggactgcgt
 3421 ggacgcgcgc ccatgttacac gaccccgagg accccccacca aacaccaaca acgcccggaaa
 3481 caccgtctgt gtcagaaaca ggcactccgt ggcacgttaca aacaacaaca tcctccctaa
 3541 cagtttacac agtaacaaag gacgggacaa caattattt acagctacgc ctgTAGttca

<- E4 end

3601 attacaaggt gatgctaatt gtttttttttggaa aaggaggccg aaaaatatgg
 3661 aacattgtttt gtagcagcat cgtccacatg ggcactccgt ggcacgttaca aacaacaaca tcctccctaa
 3721 tgcactgttta acatttttttgc acatgttgc acatgttgc acatgttgc acatgttgc
 3781 aaagtttacca ccaaaaatgtt catataaagt tggatatttgc ttttttttttgc ttttttttttgc

<- E2 end

3841 tgggttgtat atatcTAAtt gtatatttttgc tacATGgaaac acataccat agatgctact
 E5 orf start -> E5 cds ->

3901 atagggccaa ccagcacatc attactgcca gttgttatttgc ccctgtttgt atgctttgtt
 3961 agcattgttat taatttttttgc ttttttttttgc ttttttttttgc ttttttttttgc

HPV44

HPV55

LOCUS HPV55 7822 bp DNA VRL 18-JUL-1995
DEFINITION Human papillomavirus type 55, complete genome.
ACCESSION U31791
KEYWORDS .
SOURCE Human papillomavirus type 55.
REFERENCE 1 (bases 1 to 7822)
AUTHORS Delius,H.
JOURNAL Unpublished, Sequenced by Hajo Delius, Deutsches
Deutsches Krebsforschungszentrum, Angewandte Tumorvirologie,
I.N.F. 506, W-6900 Heidelberg, Germany
REFERENCE 2 (bases 1 to 7822)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1995) Andrew D. Farmer, HIV Sequence Database,
Los Alamos National Laboratory, T-10, Mail Stop K710, Los Alamos,
NM 87501, USA
COMMENT HPV-55 was first isolated from a penile condyloma acuminata. In a
survey of a large variety of tumours, HPV55 was detected in an
additional case of condyloma acuminata. Hybridization and
phylogenetic analysis group HPV-55 with HPV-44, HPV-6, HPV-11, and
HPV-13.
BASE COUNT 2400 a 1526 c 1658 g 2238 t
ORIGIN 102 bp upstream from beginning of E6 cds
1 taataataat gtaagcttta gaaaagagga gggACCGAAT TCGGTtccaA CCGAAAACGG
E2 binding -> E2 binding ->
61 TTATATAAaa accagccaa aaattaagca agcggggcat aATGgaaagt gcaaattgcct
E6 orf start -> E6 cds ->
signal ->
121 ccacggctgc acaaagtata gaccaggttgt gcaaggagggt caacattcct atgcaccatt
181 tgcaaatttt atgcgtgttt tgcaaaaaaa ccttgaccac tgcaagggtt tatttcattcg
241 catataaaaca gttatatgtt gtgttcgag gtaactttcc atttgcagcc tggccattt
301 gtttagaact acaaggttaag gtcaatcaat tttaggcattt tgacttcgat ggatatgcatt
361 taacagtggaa agaagagaca aagcagtcaa ttttggacgt gttcatacgc tggattttgt
421 gccacaaacc attgtgccac gtggaaaagg tgcgccccat attggagaag ggcgcattta
481 tTAAattaca gaatACCTGG AAGGGTcgct gttccattt ctggacatcA TGcatggaaa
E7 orf start -> -> E2 binding E7 cds ->
541 ctatcctacc tTGAAggaaa ttgtttttaga gctggatcct cctgaccctg taggcctaca
<- E6 end
601 ttgcaatgag caatttagaca gctcagagga tgagggttat gaactagcca cgcaggccac
661 gcaagacgtt acacagcctt accaaatagt aACCACCTGT GGTacatgTA AccggAACgt
E2 binding -> E1 orf start ->
721 tcggctggtt gtgcagtgc caggaacaga catctgtcaa ctacatacgc ttctgctggg
781 ttcaactggaa atactgtgtc ctgtgtgtc gcccääaaac TAAcacaGAT Ggcagacaat
<- E7 end
E1 cds ->
841 acaggtacag aggggacggg gtgctcagga tggttcttag tagaggctat agtggagaaa
901 acaactgggc aacaatatac tgaggatgag gatgaggcag tggacgatag tgggttggat
961 atgggtggact ttatagatga caggcctatt acacacaatt ccatggaaac acaggcattt
1021 ttaaacgagc aggaggcggg tgctcattat gcggctgtgc aggacctaaa acgaaagtt
1081 tttaggtatgc catatgtgag tcctttaagc aatattaagg aggcagtggaa gtgtgacatt
1141 agcccacggt tggatgccat aaaattaagt agacaACCCA AAAAGGTaaa gccgcggctg
E2 binding ->
1201 tttgaaagac cagaattaac ggacagtggaa tatggcaata ttgatgtgga agctgaaacg
1261 caggttagaga gaaatggcga accggaagat tggggggag gtggacaagg aaggcacaca
1321 gaggaggggg tggAACAGGT ggaaacggaa gtgcagacac atagcgcac acagctgcac
1381 accgagacca cgcgggtagt agaactgtta aatgtaaat atatacgggc tacactgctt
1441 ggtaaatgttta aggactgtta tgggttatca tatacagatt taattagaca attaaaaagt
1501 gacaagacaa catgtgggaa ctgggtgatt gcagcattt ggggtgcacca tagtgtatcg
1561 gaggcggttc aaaatataaatac acaaccagta acaacatataa gccacataca atggcttaca

1621 aatgcattggg gaatggtatt actggcatta ttacggttta aggtaaataa aaacagatgt
 1681 acagtggcac gcatgatggc aacacgaaa aatataccatg aggatcatat gtaattgaa
 1741 cctcctaaaa tacaaggcg tggtcagca ttatattggg tttagaagtag tatatccat
 1801 gccagtatag ttactggaga aacgcctgaa tggataacaa ggcaaaccat tggataacat
 1861 gggcttggtg acaaccaatt caaattaaca gaaatggtgc aatggcata tgataatgac
 1921 ttttgtgagg aaagtgaat tgcatttgc tatgcacaaac gtgcagatat agatgcaaat
 1981 gcaagagcat ttttaatag taattgtcag gcaaaatatg taaaagattg tgctacaatg
 2041 tgcaggact ataaaactgc agaaatgaaa aaaatgatg taaaacagtg gataaaaattt
 2101 aggaggcgt aatatgaaga aacaggcaat tggaaaccaa tagtcaatt ttaagatat
 2161 caaaaatattt aattcatcc atttttaact aaattgaaaa tggctgca tggacacct
 2221 aaaaaaaaaact gtattgcaat tggtaggacca ccagacacag ggaaatcggt tttctgtatg
 2281 agtttaatta aatttttagg aggactgtt attagttatg taaactctag tagtcacttt
 2341 tggctacagc ccctatgca tgcaaaaatgatg gcatgttgc acgtatgtac acaatcggt
 2401 tgggtatata tggatacata catgagaaac ctattagatg gaaaccctat gactattgac
 2461 agaaaacaca aatcattagc attaataaaa tggccat taatagtaac atctaacata
 2521 gacattacta aagaagatata atataaat ttatgttagca gggtaacatt attacattt
 2581 cccaaatccat tcccccttga cagaaatggg aatgcactat atgacctgtg tgaatcaaac
 2641 tggaaatgtt tctttgcaag attatcaaca agtcTAGata tacaacatc tgaggacgag
 E2 orf start ->
 2701 gacgATGgag acaatagcca agcatttgc tggctgcccag gaacagttgt tagaactgt
 E2 cds ->
 2761 TGAagaaaaat agtaataacc ttacaaaaca tatacaacat tggaaatgca taagatatga
 <- E1 end
 2821 atgtgtgttta ttacacaaag caaagcaaat gggcctaaac cacattggaa tgcaagtgg
 2881 gccagcatta acagtgtcac agacaaggg acaccaggcc attgaaatgc aatgacatt
 2941 agaaaacacta ttaaactctg actatggat ggaaccatgg acattgcaag acacaagtgc
 3001 tggaaatgtgg ttaacagcac ccaaatactg tttaaaaaaa cagggacaaa ctgtgaaatg
 3061 aaaatatgac tgcaatgcac acaacattat ggagtatgtc tcgtgaaat atatttatg
 3121 gcatgacaca gacaaatggg taaaatgtac aggacacaTA Gactataaag ggttgttata
 E4 orf start ->
 NH₂ terminus unknown
 3181 tgtacatggc gggcataaaaa cctattatac caatttgaa aaagaggcta aaaaatatgg
 3241 gaactcatta caatgggagg tctgtattgg tagcagtgtc atatgttctc ctgcatttat
 3301 atcttagtact gtcagacg tatccattgc tggcctgtc tcacacaccc cctcctccac
 3361 caccaccacc cttgcacagg cttcacctgc actgcccacc tgacccctcg aggaacgcgt
 3421 ggaccgcgc ccatgttaaac gaccccgagg acccaccaca aacaccaaca acgccaggaa
 3481 caccgtcagt gtcgcacaca gcgactccgt ggacagtaca aacaacaaca tctaccctaa
 3541 cagttacaac agtaacaaag gacgggacaa caattttgt acagctacgc ctgTAGttca
 <- E4 end
 3601 attacaaggat gatcctaatt gtttaaagtgt ttaagatat agattacatg caaagcataa
 3661 aacattgttt gtagcagcat cgtccacatg ggcgtggaca tggtcagata ctccagtaa
 3721 acatgcactg gtaacattaa catatgttaa tgaagagcaa cgtgagcagt ttttaaacac
 3781 tgtacggttt cttccaaacag ttacatataa agttggatat atgtctttac aattgttaTA
 3841 Atgcttattt tatataattTA Attgtataaa ttgtacATGg aacatataacc tatagatgg
 <- E2 end E5 orf start -> E5 cds ->
 3901 actatagggg caaccagcac atcattactg ccagttgtac ttgcctgtt tgatgtttt
 3961 gtagcattt tattaattat ttacatttct gatattttagt tgtagacatc tatattggta
 4021 ctaacccatg tgctatataat gttactttgg ctttactaa ccactgcccgt gcaattttat
 4081 gtaactaacac tgggtgtctg ctttttcct gctgtgtatc tacattctt tattgtacat
 4141 acacaagaaT AAActattaca atgctaacat gtacccatg tggatgtatg acatgggtt
 <- E5 end
 4201 tattatggtt tatattaacc ttaattgtta ccattgtggc attgttata atgcacttta
 4261 aatctgttacc atgtgttaca tgcagTAAt aagtgtttgt aaacgtgggt tggttggat
 L2 orf start ->
 4321 aattATGgca cacagcaggg cacgttagacg taaacgtgcc tcagctaccc aattatata
 L2 cds ->
 4381 aacctgttaag gctgcaggca cctgtccatc tgatattttt cctaaagttg aacataacac
 4441 tattgtgtat caaatATTAA Agtggggcag tttgggtgtt tttttggag gactggaaat
 signal ->

HPV55

7681 agccaacttt taaaagcatt tttggctact aacactacat ttttgtacag ttactgttag
7741 ttttataaaa tgagtaacct aaggcacac acctgcaACC GGTATCGGTt gaaacacacc
E2 binding ->
7801 ctgtacattt ccttattata gt

//

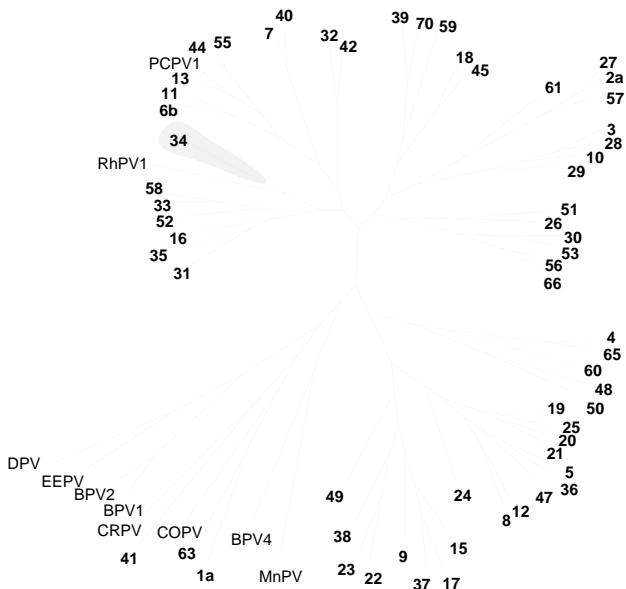
Group A11 Sequences

HPV34 HPV64
HPV73/MM9

INTRODUCTION

Group A11 is made up of three viruses (HPVs 34, 64, and 73) formerly placed in old Group B. It is a group primarily associated with orogenital lesions of low oncogenic potential. The reference clone of HPV-73 has not been released as of this writing, however, the sequence HPVMM9, treated in last year's compendium, has been found to be a variant of HPV-73.

These viruses have been predominantly linked to anogenital lesions. HPV-34 was initially isolated and cloned from a squamous cell carcinoma of Bowen's type and subsequently detected in a genital intraepithelial neoplasia and periungual Bowen's disease [1]. A study which probed lesions with Bowen's disease and squamous cell carcinomas for HPV-34 DNA, reported only one case of positive hybridization, indicating that HPV-34 infection of this nature is relatively rare [1]. HPV-64, a recently identified virus, was cloned and isolated from a vulvar intraepithelial neoplasia [2]. MM9 was derived from a genital swab specimen. Initial prevalence data for MM9 is similar to that obtained for characterized "intermediate-risk" viruses [3]. It was observed in 6 cancers (0.6%) in the IBSCC study [4], where it is referred to as PAP 238a.



What's new?

No new sequences in Group A11 were released during 1995. The sequences of members of this group were published in *Human Papillomaviruses 1994* pp. I-B-19, 26, 27, and I-I-37.

References

- [1] Kawashima,M., Jablonska,S., Favre,M., Obalek,S., Croissant,O., and Orth,G. Characterization of a new type of human papillomavirus found in a lesion of Bowen's disease of the skin. *J Virol* **57**:688-92 (1986)
- [2] de Villiers,E.M. Human pathogenic papillomavirus types: an update. in *Human pathogenic papillomaviruses*, edited by Harald zur Hausen, Springer-Verlag, Heidelberg, 1994, pp 1-12
- [3] Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger,G., Schiffmann,M., and Wheeler, C. Epidemiology and partial nucleotide sequence of four novel genital human papillomaviruses. *J Infect Dis* **170**:1096-99 (1994)
- [4] Bosch, F.X., Manos, M.M., Munoz, N., Sherman, M., Jansen, A.M., Peto, J., Schiffman, M.H., Moreno, V., Kurman, R., Shah, K.V., International Biological Study on Cervical Cancer (IBSCC) Study Group. Prevalence of human papillomavirus in cervical cancer: a worldwide perspective. *J Natl Cancer Inst* **87**:796-801 (1995)

Isolated “A” Sequences

CgPV	CP8061
HPV-54	LVX82
MM7	

This set of viruses contains supergroup A taxa that do not cluster with any groups within that supergroup.

HPV-54 and CP8061 primarily infect genital mucosa. HPV-54 was isolated from a penile Buschke-Lowenstein tumor in conjunction with HPV-6 DNA. Initial prevalence data indicates that it is a rare genital HPV type [1]. CP8061 was isolated from a cervical lavage sample obtained through clinical studies conducted in the state of New Mexico among a tri-ethnic population [2].

LVX82, which differs by only a few nucleotides from HPVMM7, was isolated from an Amazonian Indian population [3]. HPVMM7 was identified through studies conducted in the state of California. Initial prevalence data for MM7 are similar to those obtained for characterized “intermediate risk” viruses [4]. All samples were obtained from cervical lavages or genital swabs. LVX82/MM7 was detected once (0.1%) in the IBSCC study [5].

What's new?

My0911 fragments of the four human viruses CP8061, HPV-54, LVX82, and MM7 were published in *Human Papillomaviruses 1994* on pages I-F-45, I-F-40, I-E-12, and I-E-13, respectively. The complete genome of HPV-54 has become available in the past year and is published here in its entirety. The novel Colobus monkey papillomavirus (CgPV), is represented by two partial sequences, CgPV1L1 and CgPV1E1, on the following pages.

References

- [1] Favre,M., Kremsdorff,D., Jablonska,S., Obalek,S., Pehau-Arnaudet, G., Croissant, O., and Orth,G. Two new human papillomavirus types (HPV54 and 55) characterized from genital tumours illustrate the plurality of genital HPVs. *Int J Cancer* **45**: 40–46 (1990)
- [2] Peyton,C.L., and Wheeler,C.M. Identification of five novel human papillomaviruses in the New Mexico triethnic population. *J. Infect. Dis.* **170**:1089–92(1994)
- [3] Ong,C.-K., Bernard,H.-U., and Villa,L.L. Identification of genomic sequences of three novel human papillomaviruses in cervical smears of Amazonian Indians. *J. Infect. Dis.* **170**:1086–88(1994)
- [4] Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger,G., Schiffmann,M., and Wheeler, C. Epidemiology and partial nucleotide sequence of four novel genital human papillomaviruses. *J Infect Dis* **170**:1096–99 (1994)
- [5] Bosch, F.X., Manos, M.M., Munoz, N., Sherman, M., Jansen, A.M., Peto, J., Schiffman, M.H., Moreno, V., Kurman, R., Shah, K.V., International Biological Study on Cervical Cancer (IBSCC) Study Group. Prevalence of human papillomavirus in cervical cancer: a worldwide perspective. *J Natl Cancer Inst* **87**:796–801 (1995)

HPV54

HPV54

5401 gtaacaccac agttccccTA Actgcctcat cgccatatac acctataccc acatccttta
L1 orf start ->
5461 ggccctcatc aggtcacacc ccattgttc cgcacgtcc tatattcca caaacaccca
5521 ttgctgttaa tggggggat tttacctgc atcctagtt tacttatgt acaaacacgcc
5581 gtaaacgttt cccatatttt ctgcagatg gctATGtgc ggccTAGcgaa aacaaaagta
L1 cds -> <- L2 end
5641 tacctgcctc ctacccagt ttctaagggt gtcagcacgg atgaatatgt gactgcaca
5701 agcatatact atcatgcaag cagctctaga ttattggctg ttggacatcc atattttaaa
5761 gtacaaaaaaa ccaataataa gcaaagtatt cctaaagtat caggatatca atatagggt
5821 ttaggggtgc aactacctga tcctaataag tttggactgc ctgatcttag tttatataat
5881 cctgagacac aacgcttagt atgggcatgc acagggtgg aggttggtag gggccagcca
5941 ttgggtcttg gcctaagttg tcatccatta ttaaataaaat tggatgatac tgaaaatgca
6001 cctaaatatg ttggtgcaagg agctgacaat agggaaaatg ttagcatgga ctataaaca
6061 acacagttat gtattttggg ctgcacacca cctataagggt aacactggc taaaggcaac
6121 ctatgtacac ctaatacatt ggctgctggt gactgcctc ctttgaatt agtaaattca
6181 tatatacagg atggtgatata ggttagatata ggattttggg ctatggatt taaaacccta
6241 caaacctcaa aaagtggatg accccttgat gtagctacct caatttgtaa atatcctgat
6301 tacctaaaaa tggctgcaga ggcataatggg gacagtttat tttttactt aaggcgggaa
6361 caaatgtttg ttaggcatat gttaaatagg gcaggatcca tgggtgagcc tgtaccta
6421 gacttataca ttaagaaatc ctcaggtAAC cttgacaggat ctattatgc tgcaactcct
6481 agtggctcta tggtaacatc tgaataccaa atatttaata agccatactg gttacaacgg
6541 gcccagggtc aaaacaatgg tattttggg ggaatcagg tgtttttaac agttgtagat
6601 accaccctgt atractaacct aacattgtgt gctacagcat ccacgcagga tagctttaat
6661 aattctgact ttagggagta tattagacat gtggaggaat atgattaca gtttataatt
6721 cagttatgtt ccataaccct tacagcagat gttatggct atattcatgg aatgaatccc
6781 actattctag aggactggaa cttttgtata accccccccag ctacaagtag tttggaggac
6841 acatatagggt ttgtacagtc acaggccatt gcatgtcaaa agaataatgc cctgcaaaag
6901 gaaaaggagg atccttacag taaatttaat tttggactg ttgacctaa ggaacgattt
6961 tcatctgacc ttgaccagg tcccttgggt cgcaagttt tactacaggc tggctacgt
7021 gcacgtccgc gccttcggcc tgtaaaagcggt gcagccccctt cctcctctaa gggtacagcg
7081 cgcaagcggtg ctaaaactaa aaggTAACAG tggatgtatgt tggatgttta tggatgtt
-> L1 end
7141 tggatgttacc ttgtctgtgt gtatgtgtg tatgtattat gttatgtgtg gaatgttgg
7201 gtgtcctatt tatgttgtga ctcgtatgtt atatatgtt tatgtttcc tgtattat
7261 atATAAAAGa ctttgttgc accctatgag taactttgt gtatgttgc ttgctacgt
signal ->
7321 ctttagtagcc tttacctttt cacctttggt gtccattttt tataatctcc attttatata
7381 accgaaACCG TTTTCGGTtg ctgttggcac taaaactgtg ttttaagcac tttgtatcgt
E2 binding ->
7441 acatctaattt tttggggcgcc cgccacatcc tggccatggta gttttggccag cacatctgca
7501 caccacaca tttataactg tcagaacaac ttcaattttcc attgtgtaaa aacacgcct
7561 ttgcatttcca acattgattt atatatttt tacataataa aacatgttag taggcacata
7621 ttttagctgt gttaaaacttag taagtgcata gttggcaaaac taaaacatag gtgtatgcca
7681 ggtacgtgtc tggatgttgc tggatgttgc tggatgttgc tggatgttgc
E2 binding ->
7741 tcttttttat cattattat
//

LOCUS CgPV1E1 202 bp ds-DNA VRL 23-APR-1991
 DEFINITION Colobus monkey papilloma virus (CgPV-1) gene homologous to HPV-16
 E1 orf, partial cds.
 ACCESSION M64365
 SEGMENT 1 of 2
 SOURCE Colobus monkey papilloma virus (CgPV-1) DNA.
 REFERENCE 1 (bases 1 to 202)
 AUTHORS Reszka,A.A., Sundberg,J.P. and Reichmann,M.E.
 TITLE In vitro transformation and molecular characterization of colobus monkey venereal papillomavirus DNA
 JOURNAL Virology 181, 787-792 (1991)
 COMMENT The CgPV1 genome was isolated from a penile biopsy of a Colobus monkey; total length was approximately 7.8 kb. The isolated DNA was inserted into the pUC18 plasmid. Genomes obtained by *E. coli* replication of the plasmid were analysed by cross-hybridization with other PV genomes, restriction digestions, partial sequencing, and transformation assays. The greatest degree of cross-hybridization was obtained to HPVs rather than to other animal PVs, with significant hybridization under stringent conditions to HPV2a, HPV3, HPV16 and HPV18. The arrangement of the genome is similar to that of other PVs, as determined by hybridization to HPV16. Comparison of DNA sequence fragments from the E1 and L1 ORFs again showed CgPV1 to be more similar to genital HPV types than to animal PV types. The greatest similarity appears to be to Groups A2 and A4. Transformation assays indicate that CgPV1 is capable of stably transforming NIH 3T3 cells, but not C127 nor Vero cells; with respect to the 3T3 cells, transformation potential is comparable for CgPV1 and BPV1. Restriction digestion fragment sizes suggest that the genome of the CgPV1 isolate is integrated into the host's chromosomal DNA and that there has been a deletion similar to deletions found in HPV16 and HPV18 from cervical cancers. The transforming capabilities, genetic similarity of CgPV to genital HPVs, and apparent integrated and deleted state of the genome suggest that CgPV may provide a useful model for investigations of HPVs. An additional, distinct PV (CgPV-2) has been isolated from a cutaneous site on another Colobus monkey (Kloster et al. Virology 166(1):30-40).
 NCBI gi: 332158
 BASE COUNT 67 a 39 c 53 g 43 t
 ORIGIN
 1 gatggttcag tggcctacga ccacgatatac acagagagaa tttgggccta tgaatatgcc
 E1 cds ->
 61 agattagcgg atgtggatag caatgcagca gcatttttaa acagcaactg ccagGCCAAG
 NF1 bind ->
 121 tatgtaaaag atgcatgtac aatgtgcaga cattataagc gggcagaggc agcccagatg
 181 acaatgtcac aatggataag ct
 E1 cds ->
 //

CgPV

LOCUS CgPV1L1 205 bp ds-DNA VRL 23-APR-1991
DEFINITION Colobus monkey papilloma virus (CgPV-1) gene homologous to HPV-16
L1 orf, partial cds.
ACCESSION M64366
SEGMENT 2 of 2
SOURCE Colobus monkey papilloma virus (CgPV-1) DNA.
REFERENCE 1 (bases 1 to 205)
AUTHORS Reszka,A.A., Sundberg,J.P. and Reichmann,M.E.
TITLE In vitro transformation and molecular characterization of colobus monkey venereal papillomavirus DNA
JOURNAL Virology 181, 787-792 (1991)
COMMENT The CgPV1 genome was isolated from a penile biopsy of a Colobus monkey; total length was approximately 7.8 kb. The isolated DNA was inserted into the pUC18 plasmid. Genomes obtained by E. coli replication of the plasmid were analysed by cross-hybridization with other PV genomes, restriction digestions, partial sequencing, and transformation assays. The greatest degree of cross-hybridization was obtained to HPVs rather than to other animal PVs, with significant hybridization under stringent conditions to HPV2a, HPV3, HPV16 and HPV18. The arrangement of the genome is similar to that of other PVs, as determined by hybridization to HPV16. Comparison of DNA sequence fragments from the E1 and L1 ORFs again showed CgPV1 to be more similar to genital HPV types than to animal PV types. The greatest similarity appears to be to Groups A2 and A4. Transformation assays indicate that CgPV1 is capable of stably transforming NIH 3T3 cells, but not C127 nor Vero cells; with respect to the 3T3 cells, transformation potential is comparable for CgPV1 and BPV1. Restriction digestion fragment sizes suggest that the genome of the CgPV1 isolate is integrated into the host's chromosomal DNA and that there has been a deletion similar to deletions found in HPV16 and HPV18 from cervical cancers. The transforming capabilities, genetic similarity of CgPV to genital HPVs, and apparent integrated and deleted state of the genome suggest that CgPV may provide a useful model for investigations of HPVs. An additional, distinct PV (CgPV-2) has been isolated from a cutaneous site on another Colobus monkey (Kloster et al. Virology 166(1):30-40).
NCBI gi: 332159
BASE COUNT 45 a 46 c 61 g 53 t
ORIGIN
1 aagtatctgg atatcagtagt agggtgttcc gtgtcggtt tccagacccc aataagtttg
L1 cds ->
61 gtttgccccga aggctccctg tataatccag agacccaaag gtttagtatgg gcctgccgtg
121 gggtcgagggt aggtcgttggc cagcctctgg gagttggcac tagtggccat cccttggca
181 atagactggc tgacactgag aattc
L1 cds ->
//